Page 39, lines 28-29, insert:

The dissociation constants for the interaction seen between zfHAE(M), zfHHA(M) and zfHAE(T) (Table 1 F1: SEQ ID NO.:24; F2: SEQ ID NO.:29; F3: SEQ ID NO.:34) and 5-meC or T oligonucleotides are set forth in Table 3.

IN THE CLAIMS:

Kindly enter the following amended claims.

7. (Amended) The method according to claim 5 or claim 6, wherein the modified residue is 5-meC and the unmodified residue is C.

8. (Amended) The method according to claim 5 or claim 6, wherein the modified residue is U and the unmodified residue is T.

9. (Amended) The method according to claim 5 or claim 6, wherein the library is screened by phage display.

10. (Amended) The method according to claim 6, wherein each zinc finger has the primary structure of (SEQ ID NO.:40):

X^a **C** X_{2-4} **C** X_{2-3} F X^c X X X X L X X **H** X X X^b **H**- linker,

-1 1 2 3 4 5 6 7 8 9

wherein each of X, X^a, X^b and X^c is any amino acid, and

wherein X_{2-4} means either 2 or 4 amino acids are present at this position, and X_{2-3} means either 2 or 3 amino acids are present at this position.

11. (Amended) The method according to claim 10, wherein X^a is $^F/_y$-X or P-$^F/_Y$-X.

12. (Amended) The method according to claim 10 or claim 11, wherein X_{2-4} is selected from the group consisting of S-X, E-X, K-X, T-X, P-X and R-X.

13. (Amended) The method according to claim 10, wherein X^b is T or I.

14. (Amended) The method according to claim 10, wherein X_{2-3} is selected from the group consisting of G-K-A, G-K-C, G-K-S, G-K-G, M-R-N and M-R.

15. (Amended) The method according to claim 10, wherein the linker is T-G-E-K or the sequence set forth in SEQ ID NO.:3.

16. (Amended) The method according to claim 10, wherein position +9 is R or K.

17. (Amended) The method according to claim 10, wherein positions +1, +5 and +8 are not occupied by any of hydrophobic amino acids F, W or Y.

18. (Amended) The method according to claim 17, wherein positions +1, +5 and +8 are occupied by residues K, T and Q respectively.

19. (Amended) A method for preparing a DNA binding polypeptide of the Cys-2-His zinc finger class capable of binding to a DNA triplet in a target DNA sequence comprising 5-meC, but not to an identical triplet comprising unmethylated C comprising:

a) selecting a model zinc finger domain from the group consisting of naturally occurring zinc fingers and consensus fingers; and

b) mutating the finger by the method of any one of claims 3 to 5.

20. (Amended) The method according to claim 19, wherein the model zinc finger is a consensus zinc finger whose structure is selected from the group consisting of the consensus structure set forth by SEQ ID NO.:1 and the consensus structure set forth by SEQ ID NO.:2.

21. (Amended) The method according claim 19 wherein the model zinc finger domain is a naturally occurring zinc finger whose structure is selected from one finger of a protein selected from the group consisting of Zif 268, GLI, Tramtrack, and YY1.

22. (Amended) The method according to claim 21, wherein the model zinc finger is finger 2 of Zif 268.

23. (Amended) The method according to any one of claims 3, 4 or 5, wherein the binding protein comprises two or more zinc finger motifs, placed N-terminus to C-terminus.

24. (Amended) The method according to claim 22, wherein the N-terminal zinc finger is preceded by a leader peptide having the sequence of SEQ ID NO.:39.

25. (Amended) the method according to claim 23, wherein the DNA binding protein is constructed by recombinant DNA technology, the method comprising the steps of:

a) preparing a DNA coding sequence encoding two or more zinc finger binding motifs preparable according to claim 23, placed N-terminus to C-terminus;

b) inserting the DNA sequence into a suitable expression vector; and

c) expressing the DNA sequence in a host organism in order to obtain the DNA binding protein.

26. (Amended) The method according to any one of claims 3, 4 or 5 further comprising the steps of subjecting the DNA binding protein to one or more rounds of randomization and selection in order to improve the characteristics thereof.

27. (Amended) A zinc finger polypeptide which binds to a target DNA sequence containing a modified base but does not bind to an identical sequence containing the equivalent unmodified base, preparable by a method according to any one of claims 3, 4 or 5.